Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-10, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Abstract by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Kenneth A. Weber
Reg. No. 31,677

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (415) 576-0200
Fax: (415) 576-0300
KAW:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph (Table 1) beginning at line 2 of page 8 has been amended as follows (see attached sheet, Table 1):

Paragraph (Table 2) beginning at line 2 of page 10 has been amended as follows (see attached sheets, Table 2):

Paragraph (Table 3) beginning at line 2 of page 13 has been amended as follows (see attached sheet, Table 3):

Paragraph (Table 4) beginning at line 1 of page 14 has been amended as follows (see attached sheet, Table 4):

Table 1: Nucleotide sequence (SEQ ID NO:1) encoding a murine CTLA-8 protein and predicted amino acid sequence (SEQ ID NO:2). Also can use complementary nucleic acid sequences for many purposes. Submitted to GenBank/EMBL under accession number L13839.

```
   1 GAATTCCATC CATGTGCCTG ATGCTGTTGC TGCTACTGAA CCTGGAGGCT ACAGTGAAGG

  61 CAGCGGTACT CATCCCTCAA AGTTCAGTGT GTCCAAACGC CGAGGCCAAT AACTTTCTCC

 121 AGAACGTGAA GGTCAACCTG AAAGTCATCA ACTCCCTTAG CTCAAAAGCG AGCTCCAGAA

 181 GGCCCTCAGA CTACCTCAAC CGTTCCACTT CACCCTGGAC TCTGAGCCGC AATGAGGACC

 241 CTGATAGATA TCCTTCTGTG ATCTGGGAGG CACAGTGCCG CCACCAGCGC TGTGTCAACG

 301 CTGAGGGGAA GTTGGACCAC CACATGAATT CTGTTCTCAT CCAGCAAGAG ATCCTGGTCC

 361 TGAAGAGGGA GCCTGAGAAG TGCCCCTTCA CTTTCCGGGT GGAGAAGATG CTGGTGGGCG

 421 TGGGCTGCAC CTGCGTTTCC TCTATTGTCC GCCATGGGTC CTAAACAGAG ACCTGAGGCT

 481 AGCCCCTAAG AAACCCCTGC GTTTCTCTGC AAACTTCCTT GTCTTTTTAA AACAGTTCAC

 541 AGTTGAATCT CAGCAAGTGA TATGGATTTA AAGGCGGGGT TAGAATTGTC TGCCTTCCAC

 601 CCTGAAAAGA AGGCGCAGAG GGGATATAAA TTGCTTCTTG TTTTTCTGTG GGCTTTAAAT

 661 TATTTATGTA TTTACTCTAT CCCGAGATAA CTTTGAGGCA TAAGTTATTT TAATGAATTA

 721 TCTACATTAT TATTATGTTT CTTAATGCAG AAGACAAAAT TCAAGACTAA GAAATTTTAT

 781 TATTTAAAAG GTAAAACCTA TATTTATATG AGCTATTTAT GGGTCTATTT ATTTTTCTTC

 841 AGTGCTAAGA TCATGATTAT CAGATCTACC TAAGGAAGTC CTAAATAATA TTAAATATTA

 901 ATTGAAATTT CAGTTTTACT ATTTGCTTAT TTAAGGTTCC CTCCTCTGAA TGGTGTGAAA

 961 TCAAACCTCG TTTTATGTTT TTAAATTATT GAGGCTTCGA AAAATTGGGC AATTTAGCTT

1021 CCTACTGTGT GTTTAAAAAC CTTGTAACAA TATCACTATA ATAAATTTTT GGAAGAAAAT
```

Predicted amino acid sequence (150 amino acids) (SEQ ID NO:2). Mature polypeptide probably starts at about amino acid 13 (Ala).

```
MCLML LLLLN LEATV KAAVL IPQSS VCPNA EANNF LQNVK VNLKV INSLS

SKASS RRPSD YLNRS TSPWT LSRNE DPDRY PSVIW EAQCR HQRCV NAEGK

LDHHM NSVLI QQEIL VLKRE PEKCP FTFRV EKMLV GVGCT CVSSI VRHAS
```

Table 2: Nucleotide sequence (SEQ ID NO:3) of the related herpesvirus Saimiri open reading frame ORF13 and predicted amino acid sequence (SEQ ID NO:4) of encoded protein, see GenBank/EMBL accession number M60286.

herpesvirus

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTTGCAA 50

ACATGCCTCA TCTTTTGAGA AGAAACGCAA TTCGAACTTC TTCTAATGCT 100

CCTGAAGAGC AGCCTGTGCT GCAGCCTGAG CTTGATGCTA TTGAAGAGCT 150

AGAATAAGAG CTATTTTTTG ACGATGGGTG CTGCCTTTCT GTTCAAGAAA 200

TCTGCTTAAT TGTTCTTGGA TTCTTATTGT TTCTGCTAGC TGTAATTGTT 250

TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT 300

GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTACT 350

CATAATTTTA TTTTTTTATT TCTAAAACAA TCTTAGTATA TATAATTAAT 400

ACAAATTTTA GAAAATACTA TAATAAATAT TGAAAGCTGT ATTTACATTG 450

TAAACTATAT ATAGGCAATG TAAAGTCATT CTAACTTTAG GTTTGCTTTA 500

CCTGTTACAG AAACTTCACC TGTGTGTCAA GAGCTGCAAA CATGGCTTTA 550

GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT 600

GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT 650

CAACAACTGA AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC 700

ATCTCATCAC CTTCTACTTT AGAACCTTCA GAGCCTCTTA AAAACTGTAC 750

AACATTCTTA GACTTACTTT GGCAGCGGCT GGGCGAGAAC GCTTCTATAA 800

AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG AAGAATGACT 850

ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA 900

AAGACCTAGA AACTTACTGC CTACTGCTGT CGGGCCACCT CATGTCAAAT 950

ATAGACTATA TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT 1000

GGTAAACCTA TACAATTTGA TGACCCTCCT CTTCCTTATA CAGGGGCATA 1050

TAATGATGAT GGTGTTTTAA TGGTTAATAT TAATGGAAAA CATGTGAGGT 1100

TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG TACCCCATGG 1150

TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA 1200

AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG 1250

Table 2, continued:

AGCAGATTAA AGAACTAGAA AAAACTAGTA CATCTCCATA GATTACTGTT 1300

AGAATGTGTT TATCATACTA AAATAAATGC TTTATGTATT GCAATATTAC 1350

TTGTTTGCTA TGACTTTGGT ATATGAAATG CAAATCTTAA ATAAAAAGTT 1400

TTTGTCTAGT ATTGGCGTCA CTGTATTTTA CTAGCAAAAA TATATAAATT 1450

GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA 1500

CAAACATTCA ATTAGTGTAA ATCATAGCAA GCATATCTTT TCATACGTGT 1550

CTAGTTAATT TAAAGAATTA ATTATGACAT TTAGAATGAC TTCACTTGTG 1600

TTACTTCTGC TGCTGAGCAT AGATTGTATA GTAAAGTCAG AAATAACAAG 1650

CGCACAAACC CCAAGATGCT TAGCTGCTAA CAATAGCTTT CCACGGTCTG 1700

TGATGGTTAC TTTGAGCATC CGTAACTGGA ATACTAGTTC TAAAAGGGCT 1750

TCAGACTACT ACAATAGATC TACGTCTCCT TGGACTCTCC ATCGCAATGA 1800

AGATCAAGAT AGATATCCCT CTGTGATTTG GGAAGCAAAG TGTCGCTACT 1850

TAGGATGTGT TAATGCTGAT GGGAATGTAG ACTACCACAT GAACTCAGTC 1900

CCTATCCAAC AAGAGATTCT AGTGGTGCGC AAAGGGCATC AACCCTGCCC 1950

TAATTCATTT AGGCTAGAGA AGATGCTAGT GACTGTAGGC TGCACATGCG 2000

TTACTCCCAT TGTTCACAAT GTAGACTAAA AGCTATCTAA ATTTTGAAAA 2050

TTAACATTTC ACTAAAAAAC AAAAACTTGA TTTTTTTCTT TTAAATAAAA 2100

AAAGTTTAAT ATAAGTTCTG GCTTGTTTGG TTTTTGACTA ATCAATGTAG 2150

ATCACACTTG TGATCTTAGC TCTCGGGAAG CAATGTAAGA AAATATATTT 2200

AACTTAAGAG TTTTAGACTT GCTTGAGTTT TATGAGTAAA AAACAAAGAA 2250

TAAGCACAGC TTCTTGTATC TTCTTTTAAA AACTTTAAGT TATTTATGTA 2300

TTTAATATAA TCTAATGTTT CTTAAACATG TTGAGTTTGA GGTCCACTAA 2350

TACAACATTA TAATTTTTTC TGTTATAACA CTTTTGCAAG AAGAACTCAT 2400

TTTATAGAAA ATGAGCAGTA TTCAAAAAAA ATGTTTGATA TGCTGTAATA 2450

TTGGAGAGGA AGAACTTTTA CAAGCATGTG ATTGTCCTAG CAGAGTCCAT 2500

CATACATGCT TACAAAGTCA 2520

Table 2, continued:

Predicted predicted amino acid sequence (SEQ ID NO:4) of encoded protein of the related herpesvirus Saimiri open reading frame ORF13

MTFRM TSLVL LLLLS IDCIV KSEIT SAQTP RCLAA NNSFP RSVMV TLSIR 50

NWNTS SKRAS DYYNR STSPW TLHRN EDQDR YPSVI WEAKC RYLGC VNADG 100

NVDYH MNSVP IQQEI LVVRK GHQPC PNSFR LEKML VTVGC TCVTP IVHNV 150

D 151

"Table 3: Nucleotide sequence (SEQ ID NO:5) of human CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO 6) of encoded protein.

```
AGC/CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG
GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG
GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC
CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG
AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC
CAC CAT GTG GCC TAA

ser/arg asn glu asp pro glu arg tyr pro ser val ile trp glu
ala lys cys arg his leu gly cys ile asn ala asp gly asn val
asp tyr his met asn ser val pro ile gln gln glu ile leu val
leu arg arg glu pro pro his cys pro asn ser phe arg leu glu
lys ile leu val ser val gly cys thr cys val thr pro ile val
his his val ala OCH
```

This was used to isolate a full length clone from human (SEQ ID NO:7), shown below with its predicted amino acid sequence (SEQ ID NO:8); SEQ ID NO:5 corresponds to nucleotides 272-510 of SEQ ID NO:7:

```
                GG CACAAACTCA TCCATCCCCA GTTGATTGGA AGAAACAACG   42

ATG ACT CCT GGG AAG ACC TCA TTG GTG TCA CTG CTA CTG CTG CTG   87
Met thr pro gly lys thr ser leu val ser leu leu leu leu leu   15

AGC CTG GAG GCC ATA GTG AAG GCA GGA ATC ACA ATC CCA CGA AAT  132
ser leu glu ala ile val lys ala gly ile thr ile pro arg asn   30

CCA GGA TGC CCA AAT TCT GAG GAC AAG AAC TTC CCC CGG ACT GTG  177
pro gly cys pro asn ser glu asp lys asn phe pro arg thr val   45

ATG GTC AAC CTG AAC ATC CAT AAC CGG AAT ACC AAT ACC AAT CCC  222
met val asn leu asn ile his asn arg asn thr asn thr asn pro   60

aaA AGG TCC TCA GAT TAC TAC AAC CGA TCC ACC TCA CCT TGG AAT  267
lys arg ser ser asp tyr tyr asn arg ser thr ser pro trp asn   75

CTC CAC CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG  312
leu his arg asn glu asp pro glu arg tyr pro ser val ile trp   90

GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC  357
glu ala lys cys arg his leu gly cys ile asn ala asp gly asn  105

GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG  402
val asp tyr his met asn ser val pro ile gln gln glu ile leu  120

GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG  447
val leu arg arg glu pro pro his cys pro asn ser phe arg leu  135

GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT  492
glu lys ile leu val ser val gly cys thr cys val thr pro ile  150

GTC CAC CAT GTG GCC TAA                                     510
val his his val ala OCH                                     155
```

Table 4: Nucleotide sequence (SEQ ID NO:9) of mouse CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:10) of encoded protein.

gaggctcaagtgcacccagcaccagctgatcaggacgcgcaaacatgagtccagggagagcttcatctg 69

tgtctctgatgctgttgctgctgctgagcctggcggctacagtgaaggcagcagcgatcatccctcaaa 138

gctcagcgtgtccaaacactgaggccaaggacttcctccagaatgtgaaggtcaacctcaaagtcttta 207

actccgTTGGCGCAAAAGTGAGCTCCAGAAGgCCCTCAGACTACCTCAACCGTTCCACGTCACCCTGGA 276

CTCTCCACCGCAATGAAGAcCCTGATAGATATCCCTCTGTGATCTGGGAAGCTCAGTGCCGCCACCAGC 345

GCTGTGTCAATGCGGAGggaaagctggaccaccacatgaattctgttctcatccagcaagagatcctgg 414

tcctgaagagggagcctgagagctgccccttcactttcagggtcgagaagatgctggtgggTGTGGGCT 483

GCACCTGCGTGGCCTCGATTGTCCGCCAGGCAGCCTAAACAGAGACCCGCGGCTGACCCCTAAGAAACC 552

CCCACGTTTCTCAGCAAACTTACTTCCATTTTTAAAACAGTTCGTGCTATTGATTTTCAGCAAGGAATG 621

TGGATTCAGAGGCAGATTCAGAATTGTCTGCCCTCCACAATGAAAAGAAGGTGTAAAGGGGTCCCAAAC 690

TGCTTCgtgtttgtttttctgtggactttaaattatttgtgtatttacaatatccaagataactttga 759

aggcgtaacttatttaatgaagtatctacattattattatgtttctttctgaagaagacaaaattcaag 828

actcagaaattttattatttaaaaggtaagcctatatttatatgagctatttatgaatctatttatttt 897

tcttcagtatttgaagtattaagaacatgattttCAGATCTACCTAGGGAAGTCCTAAGTAAGATTAAA 966

TATTAATGGAAATTTCAGCTTTACTATTTGGTTGATTTAAGGTTCTCTCCTCTGAATGGGGTGAAAACC 1035

AAACTTAGTTTTATGTTTAATAACTTTTTAAATTATTGAAGATTCAAAAAATTGGATAATTTAGCTCCC 1104

TACTCTGTTTTAAAAAAAAAAAAAAAAAA 1134

Mouse CTLA-8 predicted amino acid sequence (SEQ ID NO:10). The mature polypeptide probably starts at a position about amino acid 19 (Leu) to amino acid 21 (Ala).

METSerProGlyArgAlaSerSerValSerLeuMETLeuLeuLeuLeuLeuSerLeuAlaAlaThrValLys 24

AlaAlaAlaIleIleProGlnSerSerAlaCysProAsnThrGluAlaLysAspPheLeuGlnAsnValLys 48

ValAsnLeuLysValPheAsnSerLeuGlyAlaLysValSerSerArgArgProSerAspTyrLeuAsnArg 72

SerThrSerProTrpThrLeuHisArgAsnGluAspProAspArgTyrProSerValIleTrpGluAlaGln 96

CysArgHisGlnArgCysValAsnAlaGluGlyLysLeuAspHisHisMETAsnSerValLeuIleGlnGln 120

GluIleLeuValLeuLysArgGluProGluSerCysProPheThrPheArgValGluLysMETLeuValGly 144

ValGlyCysThrCysValAlaSerIleValArgGlnAlaAla 158

Table 1. Nucleotide sequence (SEQ ID NO:1) encoding a murine CTLA-8 protein and predicted amino acid sequence (SEQ ID NO:2). Also can use complementary nucleic acid sequences for many purposes. Submitted to GenBank/EMBL under accession number L13339.

```
   1 GAATTCCATC CATGTGCCTG ATGCTGTTGC TGCTACTGAA CCTGGAGGCT ACAGTGAAGG

  61 CAGCGGTACT CATCCCTCAA AGTTCAGTGT GTCCAAAGGC CGAGGCCAAT AACTTTCTCC

 121 AGAACGTGAA GGTCAACCTG AAAGTCATCA ACTCCCTTAG CTCAAAAGCG AGCTCCAGAA

 181 GGCCCTCAGA CTACCTCAAC CGTTCCACTT CACCCTGGAC TCTGAGCCGC AATGAGGACC

 241 CTGATAGATA TCCTTCTGTG ATCTGGGAGG CACAGTGCCG CCACCAGCGC TGTGTCAACG

 301 CTGAGGGGAA GTTGGACCAC CACATGAATT CTGTTCTCAT CCAGCAAGAG ATCCTGGTCC

 361 TGAAGAGGGA GCCTGAGAAG TGCCCCTTCA CTTTCAGGGT GGAGAAGATG CTGGTGGCGG

 421 TGGGCTGCAC CTGCGTTTCC TCTATTGTCC GCCATGCGTC CTAAACAGAG ACCTGAGGCT

 481 AGCCCCTAAG AAACCCCTGC GTTTCTCTGC AAACTTCCTT GTCTTTTTAA AACAGTTCAC

 541 AGTTGAATCT CAGCAAGTGA TATGGATTTA AAGGCGGGGT TAGAATTGTC TGCCTTCCAC

 601 CCTGAAAAGA AGGCGCAGAG GGGATATAAA TTGCTTCTTG TTTTTCTGTG GGCTTTAAAT

 661 TATTTATGTA TTTACTCTAT CCCGAGATAA CTTTGAGGCA TAAGTTATTT TAATGAATTA

 721 TCTACATTAT TATTATGTTT CTTAATGCAG AAGACAAAAT TCAAGACTAA GAAATTTTAT

 781 TATTTAAAAG GTAAAACCTA TATTTATATG AGCTATTTAT GGGTCTATTT ATTTTTCTTC

 841 AGTGCTAAGA TCATGATTAT CAGATCTACC TAAGGAAGTC CTAAATAATA TTAAATATTA

 901 ATTGAAATTT CAGTTTTACT ATTTGCTTAT TTAAGGTTCC CTCCTCTGAA TGGTGTGAAA

 961 TCAAACCTCG TTTTATGTTT TTAAATTATT GAGGCTTCGA AAAATTGGGC AATTTAGCTT

1021 CCTACTGTGT GTTTAAAAAC CTTGTAACAA TATCACTATA ATAAATTTTT GGAAGAAAAT
```

Predicted ~~predicted~~ amino acid sequence (150 amino acids) (SEQ ID NO:2). Mature polypeptide probably starts at about amino acid 13 (Ala).

```
MCLML LLLLN LEATV KAAVL IPQSS VCPNA EANNF LQNVK VNLKV INSLS

SKASS RRPSD YLNRS TSPWT LSRNE DPDRY PSVIW EAQCR HQRCV NAEGK

LDHHM NSVLI QQEIL VLKRE PEKCP FTFRV EKMLV GVGCT CVSSI VRHAS
```

Table 2: Nucleotide sequence (SEQ ID NO:3) of the related herpesvirus Saimiri open reading frame ORF13 and predicted amino acid sequence (SEQ ID NO:4) of encoded protein, see GenBank/EMBL accession number M60286.

herpesvirus

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTTGCAA 50

ACATGCCTCA TCTTTTGAGA AGAAACGCAA TTCGAACTTC TTCTAATGCT 100

CCTGAAGAGC AGCCTGTGCT GCAGCCTGAG CTTGATGCTA TTGAAGAGCT 150

AGAATAAGAG CTATTTTTTG ACGATGGGTG CTGCCTTTCT GTTCAAGAAA 200

TCTGCTTAAT TGTTCTTGGA TTCTTATTGT TTCTGCTAGC TGTAATTGTT 250

TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT 300

GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTACT 350

CATAATTTTA TTTTTTTATT TCTAAAACAA TCTTAGTATA TATAATTAAT 400

ACAAATTTTA GAAAATACTA TAATAAATAT TGAAAGCTGT ATTTACATTG 450

TAAACTATAT ATAGGCAATG TAAAGTCATT CTAACTTTAG GTTTGCTTTA 500

CCTGTTACAG AAACTTCACC TGTGTGTCAA GAGCTGCAAA CATGGCTTTA 550

GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT 600

GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT 650

CAACAACTGA AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC 700

ATCTCATCAC CTTCTACTTT AGAACCTTCA GAGCCTCTTA AAAACTGTAC 750

AACATTCTTA GACTTACTTT GGCAGCGGCT GGGCGAGAAC GCTTCTATAA 800

AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG AAGAATGACT 850

ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA 900

AAGACCTAGA AACTTACTGC CTACTGCTGT CGGGCCACCT CATGTCAAAT 950

ATAGACTATA TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT 1000

GGTAAACCTA TACAATTTGA TGACCCTCCT CTTCCTTATA CAGGGGCATA 1050

TAATGATGAT GGTGTTTTAA TGGTTAATAT TAATGGAAAA CATGTGAGGT 1100

TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG TACCCCATGG 1150

TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA 1200

AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG 1250

Table 2, continued:

AGCAGATTAA AGAACTAGAA AAAACTAGTA CATCTCCATA GATTACTGTT 1300

AGAATGTGTT TATCATACTA AAATAAATGC TTTATGTATT GCAATATTAC 1350

TTGTTTGCTA TGACTTTGGT ATATGAAATG CAAATCTTAA ATAAAAAGTT 1400

TTTGTCTAGT ATTGGCGTCA CTGTATTTTA CTAGCAAAAA TATATAAATT 1450

GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA 1500

CAAACATTCA ATTAGTGTAA ATCATAGCAA GCATATCTTT TCATACGTGT 1550

CTAGTTAATT TAAAGAATTA ATTATGACAT TTAGAATGAC TTCACTTGTG 1600

TTACTTCTGC TGCTGAGCAT AGATTGTATA GTAAAGTCAG AAATAACAAG 1650

CGCACAAACC CCAAGATGCT TAGCTGCTAA CAATAGCTTT CCACGGTCTG 1700

TGATGGTTAC TTTGAGCATC CGTAACTGGA ATACTAGTTC TAAAAGGGCT 1750

TCAGACTACT ACAATAGATC TACGTCTCCT TGGACTCTCC ATCGCAATGA 1800

AGATCAAGAT AGATATCCCT CTGTGATTTG GGAAGCAAAG TGTCGCTACT 1850

TAGGATGTGT TAATGCTGAT GGGAATGTAG ACTACCACAT GAACTCAGTC 1900

CCTATCCAAC AAGAGATTCT AGTGGTGCGC AAAGGGCATC AACCCTGCCC 1950

TAATTCATTT AGGCTAGAGA AGATGCTAGT GACTGTAGGC TGCACATGCG 2000

TTACTCCCAT TGTTCACAAT GTAGACTAAA AGCTATCTAA ATTTTGAAAA 2050

TTAACATTTC ACTAAAAAAC AAAAACTTGA TTTTTTTCTT TTAAATAAAA 2100

AAAGTTTAAT ATAAGTTCTG GCTTGTTTGG TTTTTGACTA ATCAATGTAG 2150

ATCACACTTG TGATCTTAGC TCTCGGGAAG CAATGTAAGA AAATATATTT 2200

AACTTAAGAG TTTTAGACTT GCTTGAGTTT TATGAGTAAA AAACAAAGAA 2250

TAAGCACAGC TTCTTGTATC TTCTTTTAAA AACTTTAAGT TATTTATGTA 2300

TTTAATATAA TCTAATGTTT CTTAAACATG TTGAGTTTGA GGTCCACTAA 2350

TACAACATTA TAATTTTTTC TGTTATAACA CTTTTGCAAG AAGAACTCAT 2400

TTTATAGAAA ATGAGCAGTA TTCAAAAAAA ATGTTTGATA TGCTGTAATA 2450

TTGGAGAGGA AGAACTTTTA CAAGCATGTG ATTGTCCTAG CAGAGTCCAT 2500

CATACATGCT TACAAAGTCA 2520

Table 2, continued:

Predicted amino acid sequence (SEQ ID NO:4) of encoded protein of the related herpesvirus Saimiri open reading frame ORF13

~~Tm17.Peptide sequence~~

MTFRM TSLVL LLLLS IDCIV KSEIT SAQTP RCLAA NNSFP RSVMV TLSIR 50

NWNTS SKRAS DYYNR STSPW TLHRN EDQDR YPSVI WEAKC RYLGC VNADG 100

NVDYH MNSVP IQQEI LVVRK GHQPC PNSFR LEKML VTVGC TCVTP IVHNV 150

D 151

~~MVIDG CKKYM RRTCG DVLDN LRGDC YQVLI EDCIP VLKMY AKEGR EFDYV 50~~

~~INDLT AVPIS TSPEE DSTWD FLRLI LDLSM KVLKQ DGKTF TQGNC VNLTE 100~~

~~ALSLY EEQLG RLYCP VEFSK EIVGV PGYLE LWVFY TVWKK AKP 143~~

Table 3: Nucleotide sequence (SEQ ID NO:5) of human CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:6) of encoded protein.

```
AGC/CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG
GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG
GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC
CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG
AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC
CAC CAT GTG GCC TAA

ser/arg asn glu asp pro glu arg tyr pro ser val ile trp glu
ala lys cys arg his leu gly cys ile asn ala asp gly asn val
asp tyr his met asn ser val pro ile gln gln glu ile leu val
leu arg arg glu pro pro his cys pro asn ser phe arg leu glu
lys ile leu val ser val gly cys thr cys val thr pro ile val
his his val ala OCH
```

This ~~this~~ was used to isolate a full length clone from human (SEQ ID NO:7), shown below with its predicted amino acid sequence (SEQ ID NO:8); SEQ ID NO:5 ~~it~~ corresponds to nucleotides 272 510 of SEQ ID NO:7:

```
                GG CACAAACTCA TCCATCCCCA GTTGATTGGA AGAAACAACG   42

ATG ACT CCT GGG AAG ACC TCA TTG GTG TCA CTG CTA CTG CCG CTG   87
Met thr pro gly lys thr ser leu val ser leu leu leu leu leu   15

AGC CTG GAG GCC ATA GTG AAG GCA GGA ATC ACA ATC CCA CGA AAT  132
ser leu glu ala ile val lys ala gly ile thr ile pro arg asn   30

CCA GGA TGC CCA AAT TCT GAG GAC AAG AAC TTC CCC CGG ACT GTG  177
pro gly cys pro asn ser glu asp lys asn phe pro arg thr val   45

ATG GTC AAC CTG AAC ATC CAT AAC CGG AAT ACC AAT ACC AAT CCC  222
met val asn leu asn ile his asn arg asn thr asn thr asn pro   60

aaA AGG TCC TCA GAT TAC TAC AAC CGA TCC ACC TCA CCT TGG AAT  267
lys arg ser ser asp tyr tyr asn arg ser thr ser pro trp asn   75

CTC CAC CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG  312
leu his arg asn glu asp pro glu arg tyr pro ser val ile trp   90

GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC  357
glu ala lys cys arg his leu gly cys ile asn ala asp gly asn  105

GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG  402
val asp tyr his met asn ser val pro ile gln gln glu ile leu  120

GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG  447
val leu arg arg glu pro pro his cys pro asn ser phe arg leu  135

GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT  492
glu lys ile leu val ser val gly cys thr cys val thr pro ile  150

GTC CAC CAT GTG GCC TAA                                     510
val his his val ala OCH                                     155 ~~156~~
```

Table 4: Nucleotide sequence (SEQ ID NO:9) of mouse CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:10) of encoded protein.

gaggctcaagtgcacccagcaccagctgatcaggacgcgcaaaacatgagtccagggagagcttcatctg 69

tgtctctgatgctgttgctgctgctgagcctggcgggctacagtgaaggcagcagcgatcatccctcaaa 138

gctcagcgtgtccaaaacactgaggccaaggacttcctccagaatgtgaaggtcaacctcaaagtcttta 207

actcccTTGGCGCAAAAGTGAGCTCCAGAAGgCCCTCAGACTACCTCAACCGTTCCACGTCACCCTGGA 276

CTCTCCACCGCAATGAAGAcCCTGATAGATATCCCTCTGTGATCTGGGAAGCTCAGTGCCGCCACCAGC 345

GCTGTGTCAATGCGGAGgaaaagctggaccaccacatgaattctgttctcatccagcaagagatcctgg 414

tcctgaagagggagcctgagagctgcccattcactttcagggtcgagaagatgctggtgggTGTGGGCT 483

GCACCTGCGTGGCCTCGATTGTCCGCCAGGCAGCCTAAACAGAGACCCGCGGCTGACCCCTAAGAAACC 552

CCCACGTTTCTCAGCAAACTTACTTGCATTTTTAAAACAGTTCGTGCTATTGATTTTCAGCAAGGAATG 621

TGGATTCAGAGGCAGATTCAGAATTGTCTGCCCTCCACAATGAAAAGAAGGTGTAAAGGGGTCCCAAAC 690

TGCTTCgtgtttgtttttctgtggactttaaatttatttgtgtatttacaatatcccaagataactttga 759

aggcgtaacttatttaatgaagtatctacattattattatgtttctttctgaagaagacaaaattcaag 828

actcagaaatttttattatttaaaaggtaagcctatatttatatgagcctatttatgaaatctatttatttt 897

tcttcagtatttgaagtattaagaacatgattttCAGATCTACCTAGGGAAGTCCTAAGTAAGATTAAA 966

TATTAATGGAAATTTCAGCTTTACTATTTGGTTGATTTAAGGTTCTCTCCTCTGAATGGGGTGAAAACC 1035

AAACTTAGTTTTATGTTTAATAACTTTTTAAATTATTGAAGATTCAAAAAATTGGATAATTTAGCTCCC 1104

TACTCTGTTTTAAAAAAAAAAAAAAAAAA 1134

Mouse CTLA-8 predicted amino acid sequence (SEQ ID NO:10). The mature polypeptide probably starts at a position about amino acid 19 (Leu) to amino acid 21 (Ala).

METSerProGlyArgAlaSerSerValSerLeuMETLeuLeuLeuLeuLeuSerLeuAlaAlaThrValLys 24

AlaAlaAlaIleIleProGlnSerSerAlaCysProAsnThrGluAlaLysAspPheLeuGlnAsnValLys 48

ValAsnLeuLysValPheAsnSerLeuGlyAlaLysValSerSerArgArgProSerAspTyrLeuAsnArg 72

SerThrSerProTrpThrLeuHisArgAsnGluAspProAspArgTyrProSerValIleTrpGluAlaGln 96

CysArgHisGlnArgCysValAsnAlaGluGlyLysLeuAspHisHisMETAsnSerValLeuIleGlnGln 120

GluIleLeuValLeuLysArgGluProGluSerCysProPheThrPheArgValGluLysMETLeuValGly 144

ValGlyCysThrCysValAlaSerIleValArgGlnAlaAla 158